<u>In the Specification:</u>

On page 4, please replace the paragraph beginning on line 13 with the following:

Figures 1A-1E~~Figures 1A-1B~~ depict the nucleotide sequence of the human EPK-55053 cDNA and the corresponding amino acid sequence. The nucleotide sequence corresponds to nucleic acids 1 to 2980 of SEQ ID NO:1. The amino acid sequence corresponds to amino acids 1-778 of SEQ ID NO:2. The coding region without the 5' or 3' untranslated regions of the human EPK-55053 gene is shown in SEQ ID NO:3.

On page 4, please replace the paragraph beginning on line 20 with the following:

Figures 3A-1 – 3A-3, 3B-1 – 3B-2, and 3C~~Figures 3A-3C~~ depict the results of a search which was performed against the Washington University HMM database and which resulted in the identification of a eukaryotic protein kinase domain (SEQ ID NO:5), a UBA domain (SEQ ID NO:6), a serkin_6 domain (SEQ ID NO:7), and a tyrkin_6 domain (SEQ ID NO:8) in the amino acid sequence of human EPK-55053 (SEQ ID NO:2).

On page 5, please replace the paragraph beginning on line 27 with the following:

In another embodiment, the EPK-55053 molecules of the present invention include at least one "eukaryotic protein kinase domain". As used herein, the term "eukaryotic protein kinase domain" includes a protein domain having at least about 150-350 amino acid residues and a bit score of at least 150 when compared against a eukaryotic protein kinase domain Hidden Markov Model (HMM), *e.g.*, PFAM Accession Number PF00069. Preferably, a eukaryotic protein kinase domain includes a protein having an amino acid sequence of about 190-320, 210-300, 250-260 or more preferably about 252 amino acid residues, and a bit score of at least 150, 210, 250, 290, or more preferably, 323.4. To identify the presence of a eukaryotic protein kinase domain in an EPK-55053 protein, and make the determination that a protein of interest has a particular profile, the amino acid sequence of the protein may be searched against a database of known protein domains (*e.g.*, the HMM database). The eukaryotic protein kinase domain has been assigned the PFAM Accession No. PF00069 (see the PFAM website, available through the

University of Washington at St. Louis) and InterPro Accession No. IPR000719 (see the website for the European Bioinformatics Institute). A search was performed against the HMM database resulting in the identification of a eukaryotic protein kinase domain in the amino acid sequence of human EPK-55053 (SEQ ID NO:2) at about residues 34-285 of SEQ ID NO:2. The results of the search are set forth in <u>Figures 3A-1 − 3A-3</u><s>Figure 3A</s>.

On page 6, please replace the paragraph beginning on line 6 with the following:

In another embodiment, the isolated nucleic acid molecules of the present invention encodes at least one "ubiquitin-associated domain" or "UBA domain". As used interchangeably herein, the terms "ubiquitin-associated domain" and "UBA domain" include a protein domain having at least about 10-70 amino acid residues when compared against a UBA domain Hidden Markov Model (HMM), *e.g.*, PFAM Accession Number PF00627. Preferably, a UBA domain includes a protein having an amino acid sequence of about 10-70, 20-60, 30-50, 35-45 or more preferably about 40 amino acid residues, and a bit score of at least about 7.7. UBA domains (described in, for example, Diekmann *et al.* (1998) *Nat. Struct. Biol.* 5:1042-1047) are domains that belong to an extensive family of proteins which share a conserved sequence and which have associations with ubiquitin and the ubiquitination pathway. To identify the presence of a UBA domain in an EPK-55053 protein, and make the determination that a protein of interest has a particular profile, the amino acid sequence of the protein may be searched against a database of known protein domains (*e.g.*, the HMM database). The UBA domain has been assigned the PFAM Accession No. PF00627 (see the PFAM website, available through the University of Washington at St. Louis) and InterPro Accession No. IPR000449 (see the website for the European Bioinformatics Institute). A search was performed against the HMM database resulting in the identification of a UBA domain in the amino acid sequence of human EPK-55053 (SEQ ID NO:2) at about residues 315-356 of SEQ ID NO:2. The results of the search are set forth in <u>Figures 3A-1 − 3A-3</u><s>Figure 3A</s>.

On page 6, please replace the paragraph beginning on line 26 with the following:

To elucidate the substrate specificity of the HPK-55053 proteins of the present invention, further HMM analysis was performed using a proprietary database of Markov models, referred to

herein as the SMART HMM database (see Figures 3A-1 – 3A-3, 3B-1 – 3B-2, and 3C~~Figures 3A-3C~~). This analysis resulted in the identification of a serine threonine kinase ("serkin_6") domain at about amino acids 34-285 of the human EPK-55053 amino acid sequence set forth as SEQ ID NO:2. Notably, this serine/threonine kinase domain overlaps almost exclusively with the protein kinase domain identified by HMM searching of the PFAM database, identifying the instant proteins as serine/threonine kinases as compared to tyrosine kinases. This analysis also resulted in the identification of a tyrosine kinase domain ("tyrkin_6) at about amino acid residues 34-286 of SEQ ID NO:2.

On page 10, please replace the paragraph beginning on line 34 with the following:

The nucleotide sequence of the isolated human EPK-55053 cDNA and the predicted amino acid sequence of the human EPK-55053 polypeptide are shown in Figures 1A-1E~~Figures 1A-1B~~ and in SEQ ID NOs:1 and 2, respectively.

On page 70, please replace the paragraph beginning on line 9 with the following:

The invention is based, at least in part, on the discovery of a human gene encoding a novel polypeptide, referred to herein as human EPK-55053. The entire sequence of the human clone 55053 was determined and found to contain an open reading frame termed human "EPK-55053." The nucleotide sequence of the human EPK-55053 gene is set forth in Figures 1A-1E~~Figures 1A-1B~~ and in the Sequence Listing as SEQ ID NO:1. The amino acid sequence of the human EPK-55053 expression product is set forth in Figures 1A-1E~~Figures 1A-1B~~ and in the Sequence Listing as SEQ ID NO:2. The EPK-55053 polypeptide comprises about 778 amino acids. The coding region (open reading frame) of SEQ ID NO:1 is set forth as SEQ ID NO:3.

On page 70, please replace the paragraphs beginning on line 22 to line 30 with the following:

A search using the polypeptide sequence of SEQ ID NO:2 was performed against the HMM database in PFAM (Figures 3A-1 – 3A-3~~Figure 3A~~) resulting in the identification of a eukaryotic protein kinase domain in the amino acid sequence of human EPK-55053 at about residues 34-285 of SEQ ID NO:2 (score = 323.4). Searching the SMART HMM database

resulted in the further identification of this domain as a serine threonine kinase domain (Figures 3A-1 – 3A-3, 3B-1 – 3B-2, and 3CFigures 3A-3C).

This search also resulted in the identification of a UBA domain in the amino acid sequence of human EPK-55053 at about residues 315-356 of SEQ ID NO:2 (score = 7.7) (Figures 3A-1 – 3A-3Figure 3A).